

THE AMENDMENTS

In the Claims

1. (Currently Amended) A method for analyzing chemical genomic data, comprising:
- a). providing a database in a computer readable medium comprising at least the following four data types: (i) a plurality of standard gene expression profile informations, each profile comprising a representation of the expression level of a plurality of genes in a cell exposed to a standard compound; (ii) bioassay profiles information; (iii) gene information; and (iv) compound information for each of the plurality of standard compounds; wherein the information in any of the data types may be accessed through a query in any other data type;
 - b). ~~selecting one or more standard gene expression profiles, bioassay profiles or standard compounds~~ at least a first database record from any of the data types;
 - and
 - c). ~~using determining~~ correlation information related to the selected ~~standard gene expression profiles, bioassay profiles or standard compounds to predict a biological activity of one or more standard compounds~~ first database record;
 - d). selecting at least a second database record from the correlation information, wherein the second database record is from a different data type than the first database record;
 - e). determining product information associated with the second database record;
 - f). selecting at least one product associated with the product information;
 - wherein the product enables the user to test a hypothesis based on the correlation of the first and second database records.

2. (Previously Presented) The method of claim 1, wherein said correlation information is selected from the group consisting of: identification of one or more profiles similar to said selected standard gene expression profiles, identification of one or more standard compounds that produce a similar profile, identification of one or more genes modulated in said profile, identification of a disease or disorder in which a plurality of the same genes are modulated in a similar fashion, identification of compounds having similar physical and chemical properties as

the standard compounds used to generate the profile(s), identification of compounds having similar shapes, identification of compounds having similar biological activities, identification of a gene or protein having sequence similarity to a selected gene or protein, identification of a gene or protein having a similar known function or activity, identification of one or more genes or proteins subject to modulation or control by the same standard compound(s), identification of a gene or protein that belongs to the same metabolic or signal pathway, and identification of a gene or protein belonging to similar metabolic or signal pathways.

3. (Currently Amended) The method of claim 13, wherein said relevant product information is selected from the group consisting of: information regarding a bioassay reagent useful for measuring activity of an identified enzyme, information regarding a compound useful as a positive control, information regarding a compound useful as a negative control, information regarding a kit for purifying an identified protein, information regarding antibodies for determining and/or isolating substances, information regarding a test compound useful for further study, additional data regarding gene or protein function and/or relationships, sequence data from other species, information regarding metabolic and/or signal pathways to which the gene or protein belong, information regarding a DNA microarray useful for determining expression of the gene and/or related genes, and information and analysis regarding features of a compound that are likely to be responsible for the observed activity.

4. (Currently Amended) The method of claim 3, wherein said product information further comprises a hyperlink that facilitates direct purchase of ~~said a product~~ identified by the product information.

5. (Previously Presented) The method of claim 1, wherein said database further comprises drug signatures for a plurality of standard compounds, wherein each said drug signature comprises a representation of the physical and chemical characteristics of each compound, data regarding the effect of each compound on the transcription of a plurality of genes, data regarding the effect of each compound on a plurality of proteins and bioassay data regarding the in vivo effect of each compound.

6. (Currently Amended) The method of claim 1, wherein the first database record selected is

a standard gene expression profile is selected on the basis of its similarity to an experimental expression profile provided by the user.

7. (Currently Amended) A method for analyzing chemical genomic data, comprising:
- a) providing a database in a computer readable medium comprising drug signatures for a plurality of compounds, wherein said drug signatures comprise at least the following data types: (i) a representation of the physical and chemical characteristics of each compound; (ii) data regarding the effect of each compound on the transcription of a plurality of genes; (iii) data regarding the effect of each compound on a plurality of proteins; and (iv) bioassay data regarding the in vivo effect of each compound; wherein the information in any of the data types may be accessed through a query in any other data type;
 - b) selecting ~~one or more~~ at least one drug signatures;
and
 - c) ~~using determining~~ correlation information related to at least one data type of said one or more selected drug signatures; to predict a biological activity of one or more standard compounds
 - d) selecting at least a second drug signature based on the correlation information;
 - e) determining product information associated with the second drug signature;
 - f) selecting at least one product associated with the production information;
wherein the product enables the user to test a hypothesis based on the correlation of the first and second drug signatures.

8. (Currently Amended) The method of claim ~~14~~7, wherein said relevant product information is selected from the group consisting of: information regarding a bioassay reagent useful for measuring activity of an identified enzyme, information regarding a compound useful as a positive control, information regarding a compound useful as a negative control, information regarding a kit for purifying an identified protein, information regarding antibodies for determining and/or isolating substances, information regarding a test compound useful for further study, additional data regarding gene or protein function and/or relationships, sequence data from other species, information regarding metabolic and/or signal pathways to which the gene or

protein belong, information regarding a DNA microarray useful for determining expression of the gene and/or related genes, and information and analysis regarding features of a compound that are likely to be responsible for the observed activity.

9. (Currently Amended) The method of claim 8, wherein said product information further comprises a hyperlink that facilitates direct purchase of ~~said a product~~ identified by the product information.

10. (Currently Amended) A system for analyzing chemical genomic data, comprising:
a database in a computer readable medium comprising at least the following four data types: (i) a plurality of standard gene expression profiles information, each profile comprising a representation of the expression level of a plurality of genes in a cell exposed to a standard compound; (ii) bioassay profiles information; (iii) gene information; and (iv) compound information for each of the plurality of standard compounds; wherein the information in any of the data types may be accessed through a query in any other data type;

input means for accepting data and user selections;

selection means for selecting ~~one or more standard gene expression profiles, bioassay profiles or standard compounds~~ at least a first database record from any of the data types;

and

means for identifying and selecting correlation information related to said ~~standard gene expression profiles, bioassay profiles or standard compounds~~ that is useful to predict a biological activity of one or more standard compounds selected first database record;

selection means for selecting at least a second database record related to said first database record;

means for identifying product information associated with said second database record;

and

means for selecting at least one product associated with the product information.

11. (Previously Presented) The system of claim 10, wherein said database further comprises drug signatures for a plurality of compounds, wherein each said drug signature comprises a representation of the physical and chemical characteristics of each compound, data regarding the

effect of each compound on the transcription of a plurality of genes, data regarding the effect of each compound on a plurality of proteins, and bioassay data regarding the in vivo effect of each compound.

12. (Currently Amended) A system for ~~facilitating exploration of biological and chemical~~
analyzing chemical genomic data, comprising:

a database comprising drug signatures for a plurality of compounds, wherein each said drug signature comprises at least the following data types: (i) a representation of the physical and chemical characteristics of each compound; (ii) data regarding the effect of each compound on the transcription of a plurality of genes; (iii) data regarding the effect of each compound on a plurality of proteins; and (iv) bioassay data regarding the in vivo effect of each compound; wherein the information in any of the data types may be accessed through a query in any other data type;

input means for accepting data and user selections;

selection means for selecting ~~one or more at least one standard gene expression profiles, bioassay profiles or standard compounds~~drug signature;

and

means for identifying and selecting correlation information related to ~~said standard gene expression profiles, bioassay profiles or standard compounds~~ that is useful to predict a biological activity of one or more standard compounds at least one data type of said selected drug signature;

means for selecting at least a second drug signature based on the correlation information;

means for identifying product information associated with the second drug signature;

and

means for selecting at least one product associated with the product information.

13. (Cancelled)

14. (Cancelled)

15. (Cancelled)

16. (Cancelled)

17. (Withdrawn) A method for evaluating a test compound, comprising:
- a) providing a database in a computer readable medium comprising a plurality of standard gene expression profiles, each profile comprising a representation of the expression level of a plurality of genes in response to a standard compound, bioassay profiles and compound information for each of the standard compounds;
 - b) providing a test compound gene expression profile;
 - c) scoring the similarity of said test compound gene expression profile to the plurality of standard gene expression profiles in the database and thereby identifying at least one standard compound in the database similar to the test compound;
 - d) using correlation information related to the identified standard compound to predict a biological activity of the test compound.
18. (Withdrawn) The method of claim 17 wherein the bioassay profiles comprise data from screening assays, cellular assays, binding assays, enzymatic assays, animal studies and/or human studies.
19. (Withdrawn) The method of claim 17 wherein the bioassay profiles comprise data regarding the *in vivo* effect of each standard compound.
20. (Withdrawn) The method of claim 17 wherein the biological activity of the test compound is selected from the group consisting of drug activity, toxicity, absorption, metabolism, distribution and excretion.
21. (Withdrawn) The method of claim 17 wherein each of the plurality of standard gene expression profiles comprises a representation of the expression levels of a plurality of genes in response to the *in vivo* effect of a standard compound.
22. (Withdrawn) The method of claim 17 wherein each of the plurality of standard gene expression profiles comprises a representation of the expression levels of a plurality of genes in a particular tissue in response to the *in vivo* effect of a standard compound.